



results of BLAST

BLASTP 2.2.4 [Aug-26-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1035909885-07974-2763

Query=

(512 letters)

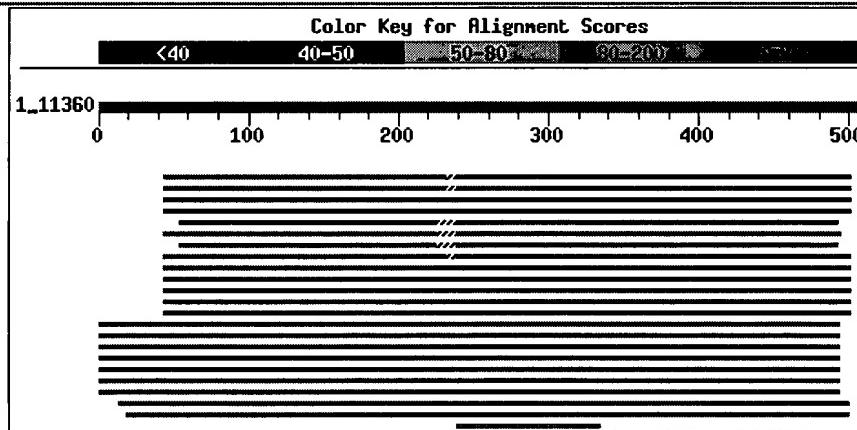
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,226,480 sequences; 390,314,779 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 662 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 337938 gb AAA64297.1	(M73240) hepatocyte growth factor ...	548	e-155	L
gi 20542440 ref XP_168542.1	(XM_168542) similar to Hepatoc... [Homo sapiens]	542	e-153	L
gi 226566 prf 1602237A	hepatocyte growth factor [Rattus no...] [Mus musculus]	535	e-151	
gi 87647 pir S06794	hepatocyte growth factor precursor (ve...) [Mus musculus]	535	e-151	
gi 18490837 gb AAH22308.1	(BC022308) Similar to hepatocyte... [Mus musculus]	514	e-144	L
gi 2135339 pir I59214	hepatocyte growth factor short form ... [Mus musculus]	509	e-143	
gi 184030 gb AAA35980.1	(M77227) competitive HGF antagonis... [Mus musculus]	509	e-143	L
gi 12583697 dbj BAB21499.1	(AB046610) hepatocyte growth fa... [Mus musculus]	506	e-142	

gi 220438 dbj BAA01065.1	(D10213) hepatocyte growth factor...	493	e-138	L
gi 433431 emb CAA51054.1	(X72307) hepatocyte growth factor...	488	e-137	L
gi 8393526 ref NP_058713.1	(NM_017017) hepatocyte growth f...	488	e-137	L
gi 632774 gb AAB31855.1	(S71816) hepatocyte growth factor;...	487	e-136	L
gi 20822586 ref XP_131908.1	(XM_131908) similar to hepatoc...	487	e-136	L
gi 1311661 gb AAC50471.1	(U37055) hepatocyte growth factor...	485	e-136	L
gi 10337615 ref NP_066278.1	(NM_020998) macrophage stimula...	485	e-136	L
gi 123114 sp P26927 HGFL HUMAN	Hepatocyte growth factor-lik...	482	e-135	
gi 90615 pir A40332	macrophage-stimulating protein 1 precu...	412	e-114	
gi 14714805 gb AAH10551.1	(BC010551) hepatocyte growth fac...	412	e-114	L
gi 6680215 ref NP_032269.1	(NM_008243) hepatocyte growth f...	410	e-113	L
gi 13242239 ref NP_077328.1	(NM_024352) macrophage stimula...	408	e-113	L
gi 1130680 emb CAA58864.1	(X84045) hepatocyte growth facto...	405	e-112	
gi 1141775 gb AAC63092.1	(U28054) hepatocyte growth factor...	403	e-111	
gi 2134350 pir I51285	hepatocyte growth factor/scatter fac...	398	e-109	
gi 1419544 emb CAA56430.1	(X80131) HGF/SF [Gallus gallus]	398	e-109	
gi 2134190 pir I51283	hepatocyte growth factor precursor -...	386	e-106	
gi 1095779 prf 2109382A	hepatocyte growth factor [Xenopus ...	386	e-106	
gi 4389172 pdb 1NK1 A	Chain A, Nk1 Fragment Of Human Hepato...	346	4e-94	
gi 1378042 gb AAC50539.1	(U46010) HGF agonist/antagonist [...	345	8e-94	L
gi 12394255 gb AAG53459.1	(M75984) hepatocyte growth facto...	345	8e-94	
gi 16975412 pdb 1GMO C	Chain C, Crystal Structures Of Nk1-H...	345	1e-93	
gi 3891529 pdb 1BHT A	Chain A, Nk1 Fragment Of Human Hepato...	340	3e-92	
gi 17942663 pdb 1GP9 C	Chain C, A New Crystal Form Of The N...	333	3e-90	
gi 11544434 emb CAC17639.1	(AL137798) dJ1182A14.3 (similar...)	317	3e-85	
gi 16758216 ref NP_445943.1	(NM_053491) plasminogen [Rattu...	314	2e-84	L
gi 2921762 gb AAC40051.1	(AF042856) hepatocyte growth fact...	311	1e-83	L
gi 2305256 gb AAB65760.1	(AF012297) plasminogen [Macropus ...	306	4e-82	
gi 1130676 emb CAA58862.1	(X84043) hepatocyte growth facto...	294	3e-78	
gi 1399751 gb AAB52574.1	(U57455) growth factor Livertine ...	281	2e-74	
gi 1619621 emb CAA69989.1	(Y08734) hepatocyte growth facto...	275	1e-72	
gi 7512243 pir T18518	apolipoprotein(a) - western European...	261	2e-68	
gi 114063 sp P14417 APOA MACMU	Apolipoprotein(a) (Apo(a)) (...)	258	2e-67	
gi 5031885 ref NP_005568.1	(NM_005577) lipoprotein, Lp(a);...	253	6e-66	L
gi 225794 prf 1313352A	apolipoprotein a [Homo sapiens]	253	6e-66	
gi 23308677 ref NP_694512.1	(NM_152980) macrophage stimula...	229	6e-59	L
gi 130319 sp P06867 PLMN PIG	Plasminogen >gi 2144494 pir P...	206	7e-52	
gi 1806583 gb AAC48717.1	(U33171) plasminogen [Erinaceus e...	205	2e-51	
gi 6708459 gb AAF25945.1	AF213397_1 (AF213397) hepatocyte g...	204	2e-51	
gi 2499860 sp Q29485 PLMN ERIEU	Plasminogen precursor >gi 2...	204	2e-51	
gi 2507247 sp P06868 PLMN BOVIN	Plasminogen precursor >gi 1...	203	4e-51	
gi 15928602 gb AAH14773.1	(BC014773) plasminogen [Mus musc...	202	9e-51	L
gi 6679381 ref NP_032903.1	(NM_008877) plasminogen [Mus mu...	200	3e-50	L
gi 190026 gb AAA36451.1	(M74220) plasminogen [Homo sapiens]	199	1e-49	L
gi 4505881 ref NP_000292.1	(NM_000301) plasminogen [Homo s...	199	1e-49	L
gi 625234 pir PLHU	plasmin (EC 3.4.21.7) precursor [valida...	199	1e-49	
gi 130317 sp P12545 PLMN MACMU	Plasminogen precursor >gi 86...	198	2e-49	
gi 3318760 pdb 2HGF	Hairpin Loop Containing Domain Of Hep...	196	5e-49	
gi 18139619 gb AAL58519.1	(AY069985) plasminogen [Canis fa...	179	8e-44	
gi 21465835 pdb 1KI0 A	Chain A, The X-Ray Structure Of Huma...	165	1e-39	
gi 2118100 pir A61545	plasmin (EC 3.4.21.7) precursor - ho...	155	9e-37	
gi 13161395 dbj BAB33031.1	(AB056447) hepatocyte growth fa...	150	6e-35	
gi 2118101 pir B61545	plasmin (EC 3.4.21.7) precursor - sh...	148	2e-34	
gi 2815616 gb AAB97886.1	(AF029691) apolipoprotein a [Papi...	145	2e-33	
gi 387031 gb AAA60124.1	(K02922) plasminogen [Homo sapiens]	137	3e-31	
gi 12394256 gb AAG53460.1	(M75984) hepatocyte growth facto...	134	2e-30	
gi 135806 sp P00735 THRB BOVIN	Prothrombin precursor >gi 62...	119	7e-26	
gi 163755 gb AAA30781.1	(J00041) preprothrombin [Bos taurus]	118	2e-25	
gi 2653563 dbj BAA23643.1	(D63779) HGF alpha-chain [Gallus...	115	2e-24	
gi 6683108 dbj BAA89046.1	(AB028871) prothrombin [Struthio...	107	3e-22	
gi 4503635 ref NP_000497.1	(NM_000506) coagulation factor ...	107	4e-22	L
gi 1335344 emb CAA23842.1	(V00595) prothrombin [Homo sapiens]	107	5e-22	L

gi 6753798	ref NP_034298.1	(NM_010168)	coagulation factor ...	106	8e-22	L
gi 289825	gb AAA21619.1	(M81391)	thrombin [Gallus gallus]	104	3e-21	
gi 266801	sp Q01177 PLMN RAT	Plasminogen	>gi 321331 pir A4...	103	6e-21	
gi 12621076	ref NP_075213.1	(NM_022924)	coagulation factor...	102	1e-20	L
gi 5921269	emb CAB56422.1	(AJ011396)	hepatocyte growth fac...	102	1e-20	
gi 13346502	ref NP_077818.1	(NM_024492)	apolipoprotein(a) ...	100	4e-20	L
gi 627678	pir E61545	plasmin (EC 3.4.21.7)	precursor - dog...	100	9e-20	
gi 22831326	dbj BAC16209.1	(AB087137)	receptor tyrosine ki...	99	1e-19	
gi 6103600	gb AAF03680.1	(AF158663)	apolipoprotein(a) [Hom...	99	2e-19	
gi 627772	pir C61545	plasmin (EC 3.4.21.7)	precursor - goa...	98	3e-19	
gi 15825918	pdb 1I5K B	Chain B, Structure And Binding Deter...		96	1e-18	
gi 22773778	gb AAN05008.1	(AY143173)	muscle-specific recep...	96	1e-18	
gi 422541	pir A47299	rror-related receptor RTK - Pacific el...		94	4e-18	
gi 14702169	ref NP_127509.1	(NM_033011)	plasminogen activa...	94	4e-18	L
gi 4505861	ref NP_000921.1	(NM_000930)	plasminogen activat...	94	5e-18	L
gi 339834	gb AAB59510.1	(L00153)	plasminogen activator [Ho...	94	5e-18	L
gi 1079221	pir S33879	plasmin precursor - lamprey (fragments)		93	8e-18	
gi 5107603	pdb 1KIV	Recombinant Kringle Iv-10M66 VARIANT ...		93	8e-18	
gi 441174	dbj BAA00881.1	(D01096)	tissue plasminogen activ...	93	9e-18	L
gi 21730366	pdb 1JFN A	Chain A, Solution Structure Of Human...		92	1e-17	
gi 5107746	pdb 3KIV	Recombinant Kringle Iv-10M66 VARIANT ...		92	2e-17	
gi 6573460	pdb 1B2I A	Chain A, Kringle 2 Domain Of Human Pl...		92	2e-17	
gi 6103599	gb AAF03679.1	(AF158663)	apolipoprotein(a) [Hom...	92	2e-17	
gi 280728	pir A60140	plasmin (EC 3.4.21.7)	precursor - chi...	92	2e-17	
gi 2815618	gb AAB97887.1	(AF029692)	plasminogen [Papio ham...	92	2e-17	
gi 9989696	gb AAG01184.2	(AF294796)	ROR2 protein [Homo sap...	92	2e-17	
gi 13878706	sp Q01974 ROR2_HUMAN	Tyrosine-protein kinase tr...		92	2e-17	
gi 19743898	ref NP_004551.2	(NM_004560)	receptor tyrosine ...	92	2e-17	L
gi 6103598	gb AAF03678.1	(AF158663)	apolipoprotein(a) [Hom...	92	2e-17	
gi 6103597	gb AAF03677.1	(AF158663)	apolipoprotein(a) [Hom...	91	3e-17	

Alignments

Get selected sequences	Select all	Deselect all
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>gi|337938|gb|AAA64297.1| (M73240) hepatocyte growth factor [Homo sapiens]
 gi|3845413|gb|AAC71655.1| (AC004960) hepatocyte growth factor [Homo sapiens]
 Length = 723

Score = 548 bits (1412), Expect = e-155
 Identities = 263/263 (100%), Positives = 263/263 (100%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANCRTNKGGLPFTCKAFVF D K 299
 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANCRTNKGGLPFTCKAFVF D K

Sbjct: 32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANCRTNKGGLPFTCKAFVF D K 91

Query: 300 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP

Sbjct: 92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT CNG 419
 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT CNG

Sbjct: 152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT CNG 211

Query: 420 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPW CYTLDP 479
 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPW CYTLDP

Sbjct: 212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPW CYTLDP 271

Query: 480 HTRWEYCAIKTCADNTMNDTDVP 502

HTRWEYCAIKTCADNTMNDTDVP

Sbjct: 272 HTRWEYCAIKTCADNTMNDTDVP 294

Score = 201 bits (510), Expect = 3e-50
 Identities = 88/173 (50%), Positives = 115/173 (65%), Gaps = 3/173 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H Y L+EN+
 Sbjct: 115 EFIDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRG---KDLQENY 171

Query: 115 CRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEYRGAVERTESGRECNRWD 174
 CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD
 Sbjct: 172 CRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWD 231

Query: 175 LNHPHNNHPFEPGKFLDNLDDNYCRNPDPGSERPWCVYTDPNIEREFCDLPRCG 227
 PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 232 HQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCA 284

Score = 152 bits (385), Expect = 9e-36
 Identities = 84/201 (41%), Positives = 105/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 181 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNESYRGLMDHTESGKICQRWDHQTPHRH 238

Query: 101 KYTPTRL--RNGLEENFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCVT DP R++ C IK+C +
 Sbjct: 239 KFLPERYPDKGFDDNYCRNPDGQP-RPWCVTLDPHTRWEYCAIKTCADNTMNDTDVPLET 297

Query: 147 AACVWCNGEEYRGAVDRTESGRECNRWDLNHPHNPFEPEGKFLDNLDDNYCRNPDGSER 206
 C+ GE YRG V+ +G C RWD +PH H P F L +NYCRNPDGSE
 Sbjct: 298 TECIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSES 357

Query: 207 PWCVTDPNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C
 Sbjct: 358 PWCFDTDPNIRVGYCSQIPNC 378

Score = 139 bits (351), Expect = 7e-32
 Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 206 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 264

Query: 391 WCFTSNPEVRYEVCDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P R+E C I C++ EC+ GE YRG ++ +G CQRW
 Sbjct: 265 WCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNNGIPCQRW 324

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH H PE + K +NYCRNPDG PWC+T DP+ R YC+
 Sbjct: 325 DSQYPHEHDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCS 373

Score = 135 bits (341), Expect = 1e-30
 Identities = 77/173 (44%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT+ +GI CQ W S PHEH +++ KDL+ENYCRNP G E P
 Sbjct: 300 CIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSE-SP 358

Query: 391 WCFTSNPEVRYEVCD-IPQCSEV---ECMTCNESYRGLMDHTESGKICQRWDHQTP--H 444
 WCFT++P +R C IP C +C NG++Y G + T SG C WD H
 Sbjct: 359 WCFTTDPNIRVGYCSQIPNCMDMSHGQDCYRGNGKNMGNLSQTRSLTCSMWDKNMEDLH 418

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495

RH F PD ++NYCRNPD PWCYT +P W+YC I C +T

Sbjct: 419 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 468

Score = 128 bits (322), Expect = 2e-28

Identities = 75/175 (42%), Positives = 99/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125

CI QG GYRG T G+PCQ W ++P++H TP L EN+CRNPDG P

Sbjct: 300 CIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSE-SP 358

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA--CVWCNGEEYRGAVDRTESGRECNRWDLNHP--H 179

WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ WD N H

Sbjct: 359 WCFTTDPPNIRVGYSQIPNCDSHMQDCYRGNGKNMGNLSQTRSGLTCMSWDKNMEDLH 418

Query: 180 NHPF-EPGKFLDNLGDDNYCRNP-DGSERPWCYTTDPNIEREFCDLPRCGSEANP 232

H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P

Sbjct: 419 RHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 470

>gi|20542440|ref|XP_168542.1| (XM_168542) similar to Hepatocyte growth factor p factor) (SF) (Hepatopoeitin A) [Homo sapiens]

gi|123116|sp|P14210|HGF_HUMAN Hepatocyte growth factor precursor (Scatter factor) (Hepatopoeitin A)

gi|87648|pir|JH0579 hepatocyte growth factor precursor - human

gi|184032|gb|AAA52648.1| (M60718) hepatocyte growth factor [Homo sapiens]

gi|219700|dbj|BAA14348.1| (D90334) hepatocyte growth factor [Homo sapiens]

gi|306846|gb|AAA52650.1| (M29145) hepatocyte growth factor [Homo sapiens]

gi|337936|gb|AAA64239.1| (M73239) hepatocyte growth factor [Homo sapiens]

Length = 728

Score = 542 bits (1396), Expect = e-153

Identities = 263/268 (98%), Positives = 263/268 (98%), Gaps = 5/268 (1%)

Query: 240 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANCRTNKGGLPFTCKAFVFDFK 299

QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANCRTNKGGLPFTCKAFVFDFK

Sbjct: 32 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANCRTNKGGLPFTCKAFVFDFK 91

Query: 300 ARKQCLWFPFNMSGGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359

ARKQCLWFPFNMSGGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP

Sbjct: 92 ARKQCLWFPFNMSGGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 414

WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC

Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDPGQPRPWC 474

MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDPGQPRPWC

Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDPGQPRPWC 271

Query: 475 YTLDPTHTRWEYCAIKTCADNTMNDTDVP 502

YTLDPTHTRWEYCAIKTCADNTMNDTDVP

Sbjct: 272 YTLDPTHTRWEYCAIKTCADNTMNDTDVP 299

Score = 205 bits (521), Expect = 2e-51

Identities = 89/175 (50%), Positives = 118/175 (66%), Gaps = 2/175 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112

E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E

Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAAACVWCNGEEYRGAVDRTESGRECNR 172

N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R

Sbjct: 175 NYCRNPDRGEEGGPWCFITSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPGKFLDNGLDDNYCRNPDGSERPWCYTTDPNIEREFCDLPRCG 227
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C

Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCA 289

Score = 152 bits (385), Expect = 9e-36
 Identities = 84/201 (41%), Positives = 105/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H

Sbjct: 186 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNESYRGLMDHTESGKICQRWDHQTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCVTTDPAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCVT DP R++ C IK+C +

Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCVTLDPHTRWEYCAIKTCADNTMNDTDVPLET 302

Query: 147 AACVWCNGEYRGAVDRTESGRECNRWDLNHPHNPFEPEKGFLDNGLDDNYCRNPDGSER 206
 C+ GE YRG V+ +G C RWD +PH H P F L +NYCRNPDGSE

Sbjct: 303 TECIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCVTTDPNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C

Sbjct: 363 PWCFDTDPNIRVGYCSQIPNC 383

Score = 139 bits (351), Expect = 7e-32
 Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P

Sbjct: 211 CMTCNEMSYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDIPQCSE-----VECMTCNEMSYRGLMDHTESGKICQWR 438
 WC+T +P R+E C I C++ EC+ GE YRG ++ +G CQRW

Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNNGIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH H PE + K +NYCRNPDG PWC+T DP+ R YC+

Sbjct: 330 DSQYPHEHDMPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCS 378

Score = 135 bits (341), Expect = 1e-30
 Identities = 77/173 (44%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GTV+ +GI CQ W S PHEH +++ KDL+ENYCRNP G E P

Sbjct: 305 CIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCD-IPQCSEV---ECMTCNEMSYRGLMDHTESGKICQRWDHQTP--H 444
 WCFT++P +R C IP C +C NG++Y G + T SG C WD H

Sbjct: 364 WCFDTDPNIRVGYCSQIPNCMSHGQDCYRGNGKNYMGNLSQTRSLTCSMWDKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T

Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 128 bits (322), Expect = 2e-28
 Identities = 75/175 (42%), Positives = 99/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYPT--LRNGLEENFCRNPDPGDPGGP 125

CI QG GYRG+ T G+PCQ W ++P++H TP L EN+CRNPDG P

Sbjct: 305 CIQGQGEGYRGTVNTIWNNGIPCQRWDSQYPHEHDMPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ WD N H
 Sbjct: 364 WCFTTDPNIRVGYCSQIPNCDSHGDGYRNGKNMGNLSQTRSGLTCMSWDLNMEDELH 423

Query: 180 NHPF-EPGKFLLDNLDDNYCRNP-DGSERPWCYTTDPNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 424 RHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 475

>gi|226566|prf||1602237A hepatocyte growth factor [Rattus norvegicus]
 Length = 728

Score = 535 bits (1379), Expect = e-151
 Identities = 259/267 (97%), Positives = 261/267 (97%), Gaps = 5/267 (1%)

Query: 241 RKRRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCANCRTNKGKLPFTCKAFVFDKA 300
 +KRRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCANCRTN GLPFTCKAFVFDKA
 Sbjct: 33 KKRRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCANCRTNGLPFTCKAFVFDKA 92

Query: 301 RKQCLWFPPNSMSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 360
 RKQCLWFPPNSMSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW
 Sbjct: 93 RKQCLWFPPNSMSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Query: 361 SSMIPHEH----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 415
 SSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM
 Sbjct: 153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 212

Query: 416 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWY 475
 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWY
 Sbjct: 213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWY 272

Query: 476 TLDPHTRWEYCAIKTCADNTMNDTDVP 502
 TLDPHTRWEYCAIKTCADNT+NDTDVP
 Sbjct: 273 TLDPHTRWEYCAIKTCADNTVNDTDVP 299

Score = 242 bits (618), Expect = 9e-63
 Identities = 136/374 (36%), Positives = 191/374 (50%), Gaps = 38/374 (10%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNFGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNHPFEPEGKFLDNLDDNYCRNPDGSERPWCYTTDPNIEREFCDLPRCGSEANP 232
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCTLDPHTRWEYCAIKTCADNTVN 294

Query: 233 XXXXXXXQRKRRNTIHEFKSAKTTLIKIDPALKIKTKVNTADQCA-----NRC 282
 + E + T+ P + ++ + D N C
 Sbjct: 295 DTDVPMETTECIQGQGEGYRGTAINTIWNGIPCQRWDSQYPHKHDMDTPENFKCKDLRENYC 354

Query: 283 TRNKGLPFTCKAFVFDKARK--QCLWFPPNSMSGVKKEFGHEFDLYENKDYIRNCIIGK 340
 RN + F D + C P MS+G ++C G
 Sbjct: 355 -RNPDGSESPWCFTTDPNIRVGYCSQIPNCDSMSNG-----QDCYRGN 395

Query: 341 GRSYKGTVSITKSGIKCQPSSMIP--HEHSYRGKD---LQENYCRNPRGEEGGPWCFTS 395
 G++Y G +S T+SG+ C W+ + H H + D L ENYCRNP + GPWC+T
 Sbjct: 396 GKNYMGNLSQTRSGLTCMSWNKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTG 455

Query: 396 NPEVRYEVCDIPQC 409
 NP + ++ C I +C
 Sbjct: 456 NPLIPWDYCPISRC 469

Score = 151 bits (381), Expect = 2e-35
 Identities = 83/201 (41%), Positives = 104/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 186 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNESYRGLMDHTESGKICQRWDHQTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +
 Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTVNDTDVPMET 302

Query: 147 AACVWCNGEYERYGAVDRTESGRECNRWDLNHPHNPFFEPGKFLDNLGDDNYCRNPDGSER 206
 C+ GE YRG + +G C RWD +PH H P F L +NYCRNPDGSE
 Sbjct: 303 TECIQGQGEGYRGTAINTIWNGIIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCYTTDPNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C
 Sbjct: 363 PWCFTTDPNIRVGYCSQIPNC 383

Score = 140 bits (352), Expect = 6e-32
 Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 211 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P R+E C I C++ EC+ GE YRG + +G CQRW
 Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGQGEGYRGTAINTIWNGIIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH+H PE + K +NYCRNPDG PWC+T DP+ R YC+
 Sbjct: 330 DSQYPHKHDMDTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCS 378

Score = 131 bits (329), Expect = 3e-29
 Identities = 74/173 (42%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT + +GI CQ W S PH+H +++ KDL+ENYCRNP G E P
 Sbjct: 305 CIQGQGEGYRGTAINTIWNGIIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCD-IPQC---SEVECMTCNESYRGLMDHTESGKICQRWDHQTP-H 444
 WCFT++P +R C IP C + +C NG++Y G + T SG C W+ H
 Sbjct: 364 WCFTTDPNIRVGYCSQIPNCDMSNGQDCYRGNGKNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 125 bits (314), Expect = 1e-27
 Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRG T G+PCQ W ++P+ H TP L EN+CRNPDG P
 Sbjct: 305 CIQGQGEGYRGTAINTIWNGIIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ W+ N H
 Sbjct: 364 WCFTTDPNIRVGYCSQIPNCDMSNGQDCYRGNGKNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 180 NHPF-EPGKFLDNGLDDNYCRNP-DGSERPWCYTDPNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P

Sbjct: 424 RHIFWEPDA---SKLMENYCRNPDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 475

>gi|87647|pir||S06794 hepatocyte growth factor precursor (version 2) - human
gi|32082|emb|CAA34387.1| (X16323) HGF (AA 1-728) [Homo sapiens]
 Length = 728

Score = 535 bits (1379), Expect = e-151
 Identities = 259/267 (97%), Positives = 261/267 (97%), Gaps = 5/267 (1%)

Query: 241 RKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNKGKLPFTCKAFVFDKA 300
 +KRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANRCTRN GLPFTCKAFVFDKA

Sbjct: 33 KKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNNGLPFTCKAFVFDKA 92

Query: 301 RKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 360
 RKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW

Sbjct: 93 RKQCLWFPPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Query: 361 SSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 415
 SSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM

Sbjct: 153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 212

Query: 416 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDGQPRPWY 475
 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDGQPRPWY

Sbjct: 213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFFDDNYCRNPDGQPRPWY 272

Query: 476 TLDPHTRWEYCAIKTCADNTMNDTDVP 502
 TLDPHTRWEYCAIKTCADNT+NNDTDVP

Sbjct: 273 TLDPHTRWEYCAIKTCADNTVNDTDVP 299

Score = 242 bits (618), Expect = 9e-63
 Identities = 136/374 (36%), Positives = 191/374 (50%), Gaps = 38/374 (10%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E

Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECRN 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNMG YRG +D TESG+ C R

Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPNHPFEPEGKFLDNGLDDNYCRNPDGSERPWYCCTDPNIEREFCDLPRCGSEANP 232
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C

Sbjct: 235 WDHQTPHRKFLPERYPDKGFFDDNYCRNPDGQPRPWYCILDPHTRWEYCAIKTCADNTVN 294

Query: 233 XXXXXXXQRKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCA-----NRC 282
 + E + T+ P + ++ + D N C

Sbjct: 295 DTDVPMETTECIQGQGEGRGTANTIWNNGIPQRWDSQYPHKHDMPENFKCKDLRENYC 354

Query: 283 TRNKGLPFTCKAFVFDKARK--QCLWFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGK 340
 RN + F D + C P MS+G ++C G

Sbjct: 355 -RNPDGSESPWCFTTDPNIRVGYCSQIPNCMSNG-----QDCYRGN 395

Query: 341 GRSYKGTVSITKSGIKCQPSSMIP--HEHSYRGKD--LQENYCRNPRGEEGGPWCFTS 395
 G++Y G +S T+SG+ C W+ + H H + D L ENYCRNP + GPWC+T

Sbjct: 396 GKNYMGNLSQTRSGLTCSMWKNMEDLHRHIFWEPDASKLNENYCRNPDDAHGPWCYTG 455

Query: 396 NPEVRYEVCDIPQC 409

NP + ++ C I +C

Sbjct: 456 NPLIPWDYCPISRC 469

Score = 151 bits (381), Expect = 2e-35

Identities = 83/201 (41%), Positives = 104/201 (51%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H
 Sbjct: 186 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCRE----- 146
 K+ P G ++N+CRNPDG P PWCYT DP R++ C IK+C +
 Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKTCADNTVNDTDVPMET 302

Query: 147 AACVWCNGEYERYGAVDRTESGRECNRWDLNHPHNPFFEPGKFLDNLDDNYCRNPDGSER 206
 C+ GE YRG + +G C RWD +PH H P F L +NYCRNPDGSE
 Sbjct: 303 TECIQGQGEGYRGTAINTIWNNGIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSES 362

Query: 207 PWCYTTDPNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P C
 Sbjct: 363 PWCFITTDPNIRVGYSQIPNC 383

Score = 140 bits (352), Expect = 6e-32

Identities = 70/169 (41%), Positives = 90/169 (52%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 211 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQP-RP 269

Query: 391 WCFTSNPEVRYEVCDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P R+E C I C++ EC+ GE YRG + +G CQRW
 Sbjct: 270 WCYTLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGQGEGYRGTAINTIWNNGIPCQRW 329

Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCA 487
 D Q PH+H PE + K +NYCRNPDG PWC+T DP+ R YC+
 Sbjct: 330 DSQYPHKHDMDTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYS 378

Score = 131 bits (329), Expect = 3e-29

Identities = 74/173 (42%), Positives = 97/173 (55%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT + +GI CQ W S PH+H +++ KDL+ENYCRNP G E P
 Sbjct: 305 CIQGQGEGYRGTAINTIWNNGIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 391 WCFTSNPEVRYEVCD-IPQC---SEVECMTCNGESYRGLMDHTESGKICQRWDHQTP-H 444
 WCFT++P +R C IP C + +C NG++Y G + T SG C W+ H
 Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSNGQDCYRGNKGNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD ++NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 424 RHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 473

Score = 125 bits (314), Expect = 1e-27

Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRGT T G+PCQ W ++P+ H TP L EN+CRNPDG P
 Sbjct: 305 CIQGQGEGYRGTAINTIWNNGIPCQRWDSQYPHKHDMDTPENFKCKDLRENYCRNPDGSE-SP 363

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEYRGAVDRTESGRECNRWDLNHP-H 179
 WC+TTDP +R C I +C + C NG+ Y G + +T SG C+ W+ N H
 Sbjct: 364 WCFTTDPNIRVGYSQIPNCDMSNGQDCYRGNKGNYMGNLSQTRSGLTCSMWNKNMEDLH 423

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTDPNIEREFCDLPRCGSEANP 232
 H F EP + L++NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 424 RHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 475

>gi|18490837|gb|AAH22308.1| (BC022308) Similar to hepatocyte growth factor (hep scatter factor) [Homo sapiens]
Length = 285

Score = 514 bits (1323), Expect = e-144
Identities = 252/252 (100%), Positives = 252/252 (100%)

Query: 240 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 299
QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK

Sbjct: 32 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 91

Query: 300 ARKQCLWFPFPNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
ARKQCLWFPFPNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP

Sbjct: 92 ARKQCLWFPFPNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 419
WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG

Sbjct: 152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Query: 420 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWCYTLDP 479
ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWCYTLDP

Sbjct: 212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWCYTLDP 271

Query: 480 HTRWEYCAIKTC 491

HTRWEYCAIKTC

Sbjct: 272 HTRWEYCAIKTC 283

Score = 196 bits (498), Expect = 8e-49
Identities = 88/172 (51%), Positives = 115/172 (66%), Gaps = 3/172 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H Y L+EN+

Sbjct: 115 EFPLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPSSMIPHEHSYRG---KDLQENY 171

Query: 115 CRNPDPGDPGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNRWD 174
CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD

Sbjct: 172 CRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWD 231

Query: 175 LNHPHNHPFEPGKFLDNLDDNYCRNPDSERPWCYTTDPNIEREFCDLPRC 226

PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C

Sbjct: 232 HQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWCYTLDPHTRWEYCAIKTC 283

Score = 65.9 bits (159), Expect = 1e-09
Identities = 33/81 (40%), Positives = 44/81 (53%), Gaps = 6/81 (7%)

Query: 414 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQP-RP 472
C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P

Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPSSMIPHEHS---YRGKDLQENYCRNPDRGEEGGP 182

Query: 473 WCYTLDPHTRWEYCAIKTCAD 493

WC+T +P R+E C I C++

Sbjct: 183 WCFTSNPEVRYEVCDIPQCSE 203

>gi|2135339|pir||I59214 hepatocyte growth factor short form precursor - human
gi|32084|emb|CAA40802.1| (X57574) hepatocyte growth factor [Homo sapiens]
gi|184034|gb|AAA52649.1| (L02931) hepatocyte growth factor [Homo sapiens]
Length = 290

Score = 509 bits (1311), Expect = e-143
Identities = 252/257 (98%), Positives = 252/257 (98%), Gaps = 5/257 (1%)

Query: 240 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 299

QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK
 Sbjct: 32 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 91

 Query: 300 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
 Sbjct: 92 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

 Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 414
 WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
 Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

 Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC 474
 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC
 Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWC 271

 Query: 475 YTLDPTHTRWEYCAIKTC 491
 YTLDPTHTRWEYCAIKTC
 Sbjct: 272 YTLDPTHTRWEYCAIKTC 288

Score = 200 bits (509), Expect = 3e-50
 Identities = 89/174 (51%), Positives = 118/174 (67%), Gaps = 2/174 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFNDHYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E
 Sbjct: 115 EFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

 Query: 113 NFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAAACVWCNGEEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

 Query: 173 WDLNHPHNHPFEPEGKFLDNGLDDNYCRNPDSERPWCYTTDPNIEREFCDLPRC 226
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 235 WDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQPRPWCYTLDPHTRWEYCAIKTC 288

Score = 78.2 bits (191), Expect = 3e-13
 Identities = 36/81 (44%), Positives = 47/81 (57%), Gaps = 1/81 (1%)

Query: 414 CMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDPGQP-RP 472
 C+ G SY+G + T+SG CQ W PH H FLP Y K +NYCRNP G+ P
 Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGP 187

 Query: 473 WCYTLDPTHTRWEYCAIKTCAD 493
 WC+T +P R+E C I C++
 Sbjct: 188 WCFTSNPEVRYEVCDIPQCSE 208

>gi|184030|gb|AAA35980.1| (M77227) competitive HGF antagonist [Homo sapiens]
 Length = 296

Score = 509 bits (1311), Expect = e-143
 Identities = 252/261 (96%), Positives = 252/261 (96%), Gaps = 5/261 (1%)

Query: 240 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 299
 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK
 Sbjct: 32 QRKRRNTIHEFKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNRNKGGLPFTCKAFVFDK 91

 Query: 300 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359
 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
 Sbjct: 92 ARKQCLWFPFNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

 Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 414
 WSSMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC
 Sbjct: 152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 474
 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC

Sbjct: 212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Query: 475 YTLDPTHTRWEYCAIKTCADNT 495

YTLDPTHTRWEYCAIK D T

Sbjct: 272 YTLDPTHTRWEYCAIKNMRDIT 292

Score = 199 bits (506), Expect = 7e-50

Identities = 88/169 (52%), Positives = 116/169 (68%), Gaps = 2/169 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFNPNDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ WS P++H + P+ G L+E

Sbjct: 115 EFIDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQE 174

Query: 113 NFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R

Sbjct: 175 NYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQR 234

Query: 173 WDLNHPHNPFEPEGKFLDNLDDNYCRNPDGSERPWCYTTDPNIEREF 221

WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C

Sbjct: 235 WDHQTPHRKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYC 283

Score = 76.6 bits (187), Expect = 8e-13

Identities = 44/108 (40%), Positives = 57/108 (52%), Gaps = 8/108 (7%)

Query: 44 GPW---QEDVADAEECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFNPNDH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W H+ P+ H

Sbjct: 186 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 243

Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCRE 146

K+ P G ++N+CRNPDG P PWCVT DP R++ C IK+ R+

Sbjct: 244 KFLPERYPDKGFDDNYCRNPDGQP-RPWCYTLDPHTRWEYCAIKNMRD 290

Score = 76.3 bits (186), Expect = 1e-12

Identities = 34/79 (43%), Positives = 46/79 (58%), Gaps = 1/79 (1%)

Query: 149 CWVCNGEEYRGAVDRTESGRECNRWDLNHPHNHFEPGKFLDNLDDNYCRNPDGSE-RP 207

C+ G Y+G V T+SG +C W PH H F P + L +NYCRNP G E P

Sbjct: 128 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGP 187

Query: 208 WCYTTDPNIEREFCDLPRC 226

WC+T++P + E CD+P+C

Sbjct: 188 WCFTSNPEVRYEVCDIPQC 206

>gi|12583697|dbj|BAB21499.1| (AB046610) hepatocyte growth factor HGF [Felis catus]
gi|22335679|dbj|BAC10545.1| (AB080187) hepatocyte growth factor [Felis catus]
 Length = 728

Score = 506 bits (1303), Expect = e-142

Identities = 245/268 (91%), Positives = 253/268 (93%), Gaps = 5/268 (1%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNKGLPFTCKAFVFDK 299

Q+KRRNT+HEFKKSAKTTLIK DP LKIKTKK+NTADQCANRC RNKGLPFTCKAFVFDK

Sbjct: 30 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKMMNTADQCANRCIRNKGLPFTCKAFVFDK 89

Query: 300 ARKQCLWFPNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 359

ARK+CLWFPNSM+SGVKKEFGHEFDLYENKDYIRNCIIGKG SYKGTVSITKSGIKCQP

Sbjct: 90 ARKRCLWFPNSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 149

Query: 360 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 414

W+SMIPHEH SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC

Sbjct: 150 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209
 Query: 415 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPW 474
 MTCNGESYRG MDHTESGKICQRWD QTPHRHKFLPERYPDKGFDDNYCRNPDG+PRPW
 Sbjct: 210 MTCNGESYRGPMMDHTESGKICQRWDRQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPW 269
 Query: 475 YTLDPHTRWEYCAIKTCADNTMNDTDVP 502
 YTLD P T WEYCAIK CA +TMNDTDVP
 Sbjct: 270 YTLDPTPWEYCAIKMCAHSTMNDTDVP 297

Score = 203 bits (517), Expect = 4e-51
 Identities = 88/175 (50%), Positives = 118/175 (67%), Gaps = 2/175 (1%)

Query: 55 ECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFQPNHDHKYTPTLRNG--LEE 112
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ W+ P++H + P+ G L+E
 Sbjct: 113 EFIDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQPWNSMIPHEHSFLPSSYRGKDLQE 172
 Query: 113 NFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNR 172
 N+CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C R
 Sbjct: 173 NYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGPMMDHTESGKICQR 232
 Query: 173 WDLNHPHNHPFEPGKFLDNLDDNYCRNPDGSERPWCYTTDPNIEREFCDLPRCG 227
 WD PH H F P ++ D G DDNYCRNPDG RPWCYT DP+ E+C + C
 Sbjct: 233 WDRQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWCYTLDPTPWEYCAIKMCA 287

Score = 144 bits (363), Expect = 3e-33
 Identities = 79/201 (39%), Positives = 103/201 (50%), Gaps = 21/201 (10%)

Query: 44 GPW---QEDVADAEECDLFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFQPNH 100
 GPW E CD+ Q + C+ G YRG M T G CQ W + P+ H
 Sbjct: 184 GPWCFTSNPEVRYEVCDIPQCSEV--ECMTCNGESYRGPMMDHTESGKICQRWDRQTPHRH 241
 Query: 101 KYTPTL--RNGLEENFCRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAA----- 148
 K+ P G ++N+CRNPDG P PW CYT DP ++ C IK C +
 Sbjct: 242 KFLPERYPDKGFDDNYCRNPDGKP-RPWCYTLDPTPWEYCAIKMCAHSTMNDTDVPMET 300
 Query: 149 --CWVCNGEEYRGAVDRTESGRECNRWDLNHPHNPFEPGKFLDNLDDNYCRNPDGSER 206
 C+ GE YRG ++ +G C RWD +PH H P F L +N+CRNPDG+E
 Sbjct: 301 TECIQGQGEGYRGRTINSIWNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDAES 360
 Query: 207 PW CYTTDPNIEREFCD-LPRC 226
 PWC+TTDPNI +C +P+C
 Sbjct: 361 PWCFDTDPNIRVGYCSQIPKC 381

Score = 136 bits (342), Expect = 9e-31
 Identities = 68/169 (40%), Positives = 90/169 (53%), Gaps = 18/169 (10%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS----YRGKDLQENYCRNPRGEEGGP 390
 C+ G SY+G + T+SG CQ W PH H Y K +NYCRNP G+ P
 Sbjct: 209 CMTCNGESYRGPMMDHTESGKICQRWDRQTPHRHKFLPERYPDKGFDDNYCRNPDGKP-RP 267
 Query: 391 WCFTSNPEVRYEVCDIPQCSE-----VECMTCNGESYRGLMDHTESGKICQRW 438
 WC+T +P+ +E C I C+ EC+ GE YRG ++ +G CQRW
 Sbjct: 268 WCYTLDPTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGRTINSIWNGVPCQRW 327
 Query: 439 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPTRWEYCA 487
 D Q PH+H PE + K +N+CRNPDG PWC+T DP+ R YC+
 Sbjct: 328 DSQYPHQHDITPENFKCKDLRENFCRNPDAESPWCFTTDPNIRVGYCS 376

Score = 130 bits (327), Expect = 5e-29
 Identities = 73/173 (42%), Positives = 98/173 (56%), Gaps = 17/173 (9%)

Query: 336 CIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEH----SYRGKDLQENYCRNPRGEEGGP 390
 CI G+G Y+GT++ +G+ CQ W S PH+H +++ KDL+EN+CRNP G E P
 Sbjct: 303 CIQQGEGYRGTINSIWNNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDGAE-SP 361

Query: 391 WCFTSNPEVRYEVCD-IPQC---SEVECMTCNGESYRGLMDHTESGKICQRWDHQTP--H 444
 WCFT++P +R C IP+C S +C NG++Y G + T SG C W+ H
 Sbjct: 362 WCFTTDPNIRVGYCSQIPKCDVSSGQDCYRNGKNMGNLSKTRSGLTCMSWEKNMEDLH 421

Query: 445 RHKFLPERYPDKG-FDDNYCRNPDGQPR-PWCYTLDPHTRWEYCAIKTCADNT 495
 RH F PD + NYCRNPD PWCYT +P W+YC I C +T
 Sbjct: 422 RHIFWE---PDASKLNKNYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 471

Score = 125 bits (314), Expect = 1e-27
 Identities = 74/175 (42%), Positives = 97/175 (55%), Gaps = 14/175 (8%)

Query: 68 CIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPT--LRNGLEENFCRNPDPGDPGGP 125
 CI QG GYRGT+ + G+PCQ W ++P+ H TP L ENFCRNPDPG P
 Sbjct: 303 CIQQGEGYRGTINSIWNNGVPCQRWDSQYPHQHDITPENFKCKDLRENFCRNPDGAE-SP 361

Query: 126 WCYTTDPAVRFQSCG-IKSCREAA---CVWCNGEEYRGAVDRTESGRECNRWDLNHP--H 179
 WC+TTDP +R C I C ++ C NG+ Y G + +T SG C+ W+ N H
 Sbjct: 362 WCFTTDPNIRVGYCSQIPKCDVSSGQDCYRNGKNMGNLSKTRSGLTCMSWEKNMEDLH 421

Query: 180 NHPF-EPGKFLDNLDDNYCRNP-DGSERPWCYTTDPNIEREFCDLPRCGSEANP 232
 H F EP + L+ NYCRNP D + PWCYT +P I ++C + RC + P
 Sbjct: 422 RHIFWEPDA---SKLNKNYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 473

>gi|220438|dbj|BAA01065.1| (D10213) hepatocyte growth factor precursor [Mus mus
 Length = 723

Score = 493 bits (1269), Expect = e-138
 Identities = 234/263 (88%), Positives = 247/263 (92%)

Query: 240 QRKRRNTIHEFKKSAKTTLIKIDPALIKTKVVNTADQCANRCTRNKGLPFTCKAFVFDK 299
 Q+KRRNT+HEFKKSAKTTL K DP LKIKTKVVN+AD+CANRC RN+G FTCKAFVFDK
 Sbjct: 33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKVVNSADECANRCIRNRGFTFTCKAFVFDK 92

Query: 300 ARKQCLWFPNSMSSGVKEFGHEFDLYENKDYIRNCIIIGKGRSYKGTVSITKSGIKCQP 359
 +RK+C W+PFNSMSSGVKK FGHEFDLYENKDYIRNCIIIGKG SYKGTVSITKSGIKCQP
 Sbjct: 93 SRKRCYWPFNSMSSGVKKFGHEFDLYENKDYIRNCIIIGGGSYKGTVSITKSGIKCQP 152

Query: 360 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 419
 W+SMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG
 Sbjct: 153 WNSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 212

Query: 420 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDGFDDNYCRNPDPGQPRPWCYTLDP 479
 ESYRG MDHTESGK CQRWD QTPHRHKFLPERYPDGFDDNYCRNPDPG+PRPWCYTLDP
 Sbjct: 213 ESYRGPMDDHTESGKTCQRWDQQTPHRHKFLPERYPDGFDDNYCRNPDPGKPRPWCYTLDP 272

Query: 480 HTRWEYCAIKTCADNTMNDTDVP 502
 T WEYCAIKTC + +N+TDVP
 Sbjct: 273 DTPWEYCAIKTCAHSAVNEDVP 295

Score = 238 bits (606), Expect = 2e-61
 Identities = 135/372 (36%), Positives = 187/372 (49%), Gaps = 39/372 (10%)

Query: 55 ECDFQKKDYVRTCIMQQGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENF 114
 E DL++ KDY+R CI+ +G Y+GT++ T G+ CQ W+ P++H Y L+EN+
 Sbjct: 116 EFDTLYENKDYIRNCIIIGGGSYKGTVSITKSGIKCQPWNSMIPHEHSYRG---KDLQENY 172

Query: 115 CRNPDPGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECNRW 174
 CRNP G+ GGPWC+T++P VR++ C I C E C+ CNGE YRG +D TESG+ C RWD